

RWorksheet_Calatana_4B

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```
vectorA <- c(1, 2, 3, 4, 5)
matrixA <- matrix(0, nrow = 5, ncol = 5)
print(matrixA)
```

```
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    0    0    0    0    0
## [2,]    0    0    0    0    0
## [3,]    0    0    0    0    0
## [4,]    0    0    0    0    0
## [5,]    0    0    0    0    0
```

```
for (i in 1:5) {
  for (j in 1:5) {
    matrixA[i, j] <- abs(vectorA[i] - vectorA[j])
  }
}
```

```
print(matrixA)
```

```
##      [,1] [,2] [,3] [,4] [,5]
## [1,]    0    1    2    3    4
## [2,]    1    0    1    2    3
## [3,]    2    1    0    1    2
## [4,]    3    2    1    0    1
## [5,]    4    3    2    1    0
```

```
num_lines <- 5
```

```
for (i in 1:num_lines) {
  for (j in 1:i) {
    cat("*")
  }
  cat("\n")
}
```

```
## *
## **
## ***
## ****
## *****
```

```
input_number <- as.numeric(readline("Enter a number to start the Fibonacci sequence: "))
```

```
## Enter a number to start the Fibonacci sequence:
```

```
assume_number <- 0
a <- 0
b <- 1
```

```
repeat {

  if (a > 500) {
    break
  }

  if (a >= assume_number) {
    cat(a, " ")
  }

  temp <- a + b
  a <- b
  b <- temp
}
```

```
## 0 1 1 2 3 5 8 13 21 34 55 89 144 233 377
```

```
cat("\n")
```

```
shoenga <- read.csv("Shoe_sizes.csv")
shoenga
```

```
##      Shoe.size Height Gender Shoe.size.1 Height.1 Gender.1
## 1         6.5   66.0      F         13.0       77         M
## 2         9.0   68.0      F         11.5       72         M
## 3         8.5   64.5      F          8.5       59         F
## 4         8.5   65.0      F          5.0       62         F
## 5        10.5   70.0      M         10.0       72         M
## 6         7.0   64.0      F          6.5       66         F
## 7         9.5   70.0      F          7.5       64         F
## 8         9.0   71.0      F          8.5       67         M
## 9        13.0   72.0      M         10.5       73         M
## 10        7.5   64.0      F          8.5       69         F
## 11        10.5   74.5      M         10.5       72         M
## 12         8.5   67.0      F         11.0       70         M
## 13        12.0   71.0      M          9.0       69         M
## 14        10.5   71.0      M         13.0       70         M
```

```
shoenganga <- shoenga[c(1:6),]
shoenganga
```

```
##      Shoe.size Height Gender Shoe.size.1 Height.1 Gender.1
## 1         6.5   66.0      F         13.0       77         M
## 2         9.0   68.0      F         11.5       72         M
## 3         8.5   64.5      F          8.5       59         F
## 4         8.5   65.0      F          5.0       62         F
## 5        10.5   70.0      M         10.0       72         M
## 6         7.0   64.0      F          6.5       66         F
```

```
female_data <- subset(shoenga, Gender == "F")
female_data
```

```
##      Shoe.size Height Gender Shoe.size.1 Height.1 Gender.1
## 1      6.5   66.0      F      13.0      77      M
## 2      9.0   68.0      F      11.5      72      M
## 3      8.5   64.5      F       8.5      59      F
## 4      8.5   65.0      F       5.0      62      F
## 6      7.0   64.0      F       6.5      66      F
## 7      9.5   70.0      F       7.5      64      F
## 8      9.0   71.0      F       8.5      67      M
## 10     7.5   64.0      F       8.5      69      F
## 12     8.5   67.0      F      11.0      70      M
```

```
male_data <- subset(shoenga, Gender == "M")
male_data
```

```
##      Shoe.size Height Gender Shoe.size.1 Height.1 Gender.1
## 5      10.5   70.0      M      10.0      72      M
## 9      13.0   72.0      M      10.5      73      M
## 11     10.5   74.5      M      10.5      72      M
## 13     12.0   71.0      M       9.0      69      M
## 14     10.5   71.0      M      13.0      70      M
```

```
nrow(female_data)
```

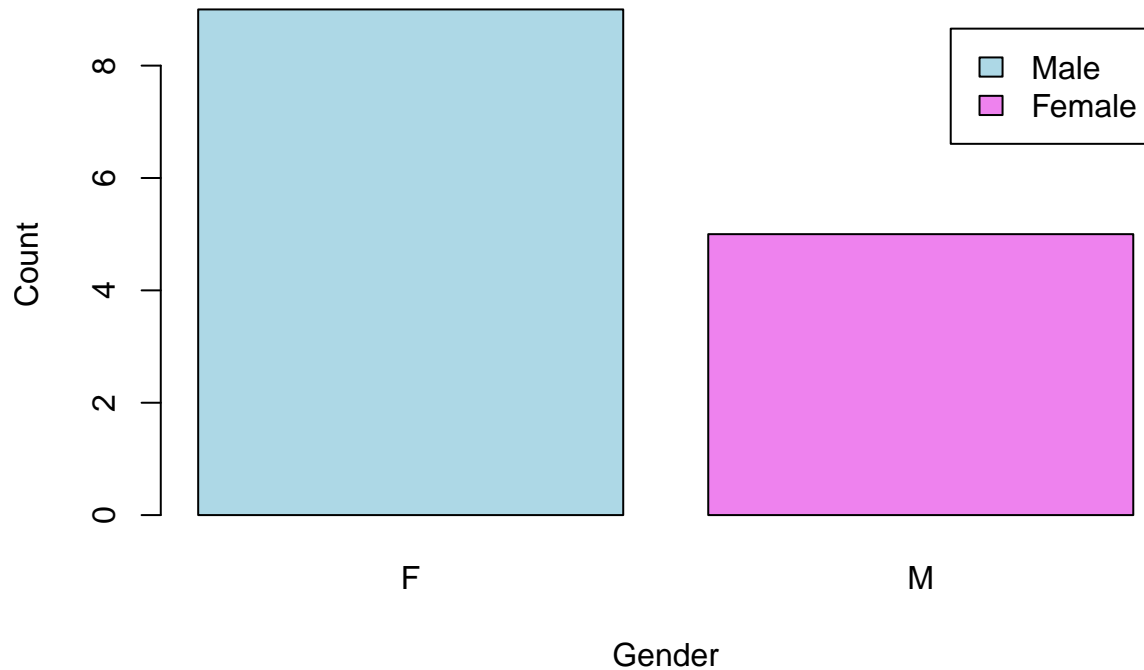
```
## [1] 9
```

```
nrow(male_data)
```

```
## [1] 5
```

```
GraphMF<- table(shoenga$Gender)
barplot(GraphMF,
  main = "Number of Males and Females",
  xlab = "Gender",
  ylab = "Count",
  col = c("lightblue", "violet"),
  legend.text = c("Male", "Female"),
  beside = TRUE
)
```

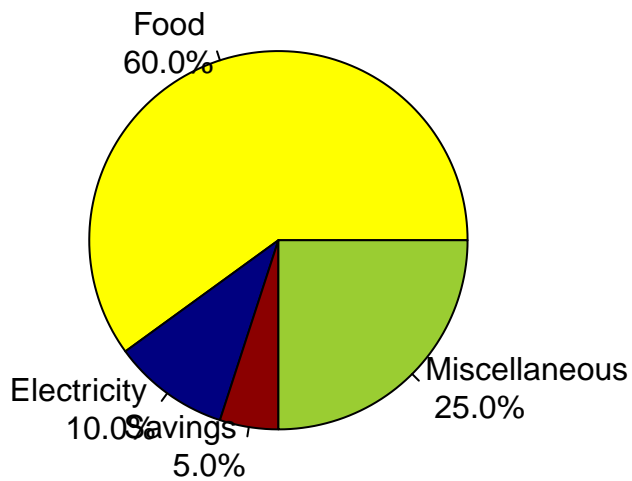
Number of Males and Females



```
Expenses <- c(Food = 60, Electricity = 10, Savings = 5, Miscellaneous = 25)

pie(Expenses,
  labels = paste(names(Expenses), "\n", sprintf("%.1f%", prop.table(Expenses) * 100)),
  col = c("yellow", "navyblue", "darkred", "yellowgreen"),
  main = "Monthly Expenses of the Dela Cruz Family"
)
```

Monthly Expenses of the Dela Cruz Family



```
data("iris")
str(iris)
```

```
## 'data.frame': 150 obs. of 5 variables:
## $ Sepal.Length: num 5.1 4.9 4.7 4.6 5 5.4 4.6 5 4.4 4.9 ...
## $ Sepal.Width : num 3.5 3 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 ...
## $ Petal.Length: num 1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 ...
## $ Petal.Width : num 0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 ...
## $ Species : Factor w/ 3 levels "setosa","versicolor",...: 1 1 1 1 1 1 1 1 1 1 ...

#The iris dataset has 150 observations and 5 variables.
#These variables are the Sepal.Length, Sepal.Width, Petal.Length, Petal.Width, and Species.

MeanIris<- colMeans(iris[, c("Sepal.Length", "Sepal.Width", "Petal.Length", "Petal.Width")])
print(MeanIris)

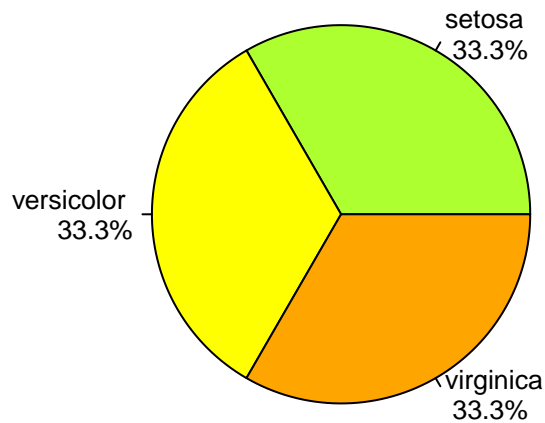
## Sepal.Length Sepal.Width Petal.Length Petal.Width
## 5.843333 3.057333 3.758000 1.199333

Spec <- table(iris$Species)

clors <- c("greenyellow", "yellow", "orange")

pie(Spec,
    labels = paste(names(Spec), "\n", sprintf("%.1f%%", prop.table(Spec) * 100)),
    col = clors,
    main = "Species Distribution",
    cex.main = 1.5,
    cex = 0.8
)
```

Species Distribution



```
SetosaSub <- subset(iris, Species == "setosa")
VersiSub <- subset(iris, Species == "versicolor")
VirgiSub <- subset(iris, Species == "virginica")

# Display the last six rows of each species
cat("Last six rows of Setosa:")
```

```
## Last six rows of Setosa:
```

```
print(tail(SetosaSub))
```

```
##      Sepal.Length Sepal.Width Petal.Length Petal.Width Species
## 45          5.1         3.8          1.9         0.4   setosa
## 46          4.8         3.0          1.4         0.3   setosa
## 47          5.1         3.8          1.6         0.2   setosa
## 48          4.6         3.2          1.4         0.2   setosa
## 49          5.3         3.7          1.5         0.2   setosa
## 50          5.0         3.3          1.4         0.2   setosa
```

```
cat("Last six rows of Versicolor:")
```

```
## Last six rows of Versicolor:
```

```
print(tail(VersiSub))
```

```
##      Sepal.Length Sepal.Width Petal.Length Petal.Width   Species
## 95          5.6         2.7         4.2         1.3 versicolor
## 96          5.7         3.0         4.2         1.2 versicolor
## 97          5.7         2.9         4.2         1.3 versicolor
## 98          6.2         2.9         4.3         1.3 versicolor
## 99          5.1         2.5         3.0         1.1 versicolor
## 100         5.7         2.8         4.1         1.3 versicolor
```

```
cat("Last six rows of Virginica:")
```

```
## Last six rows of Virginica:
```

```
print(tail(VirgiSub))
```

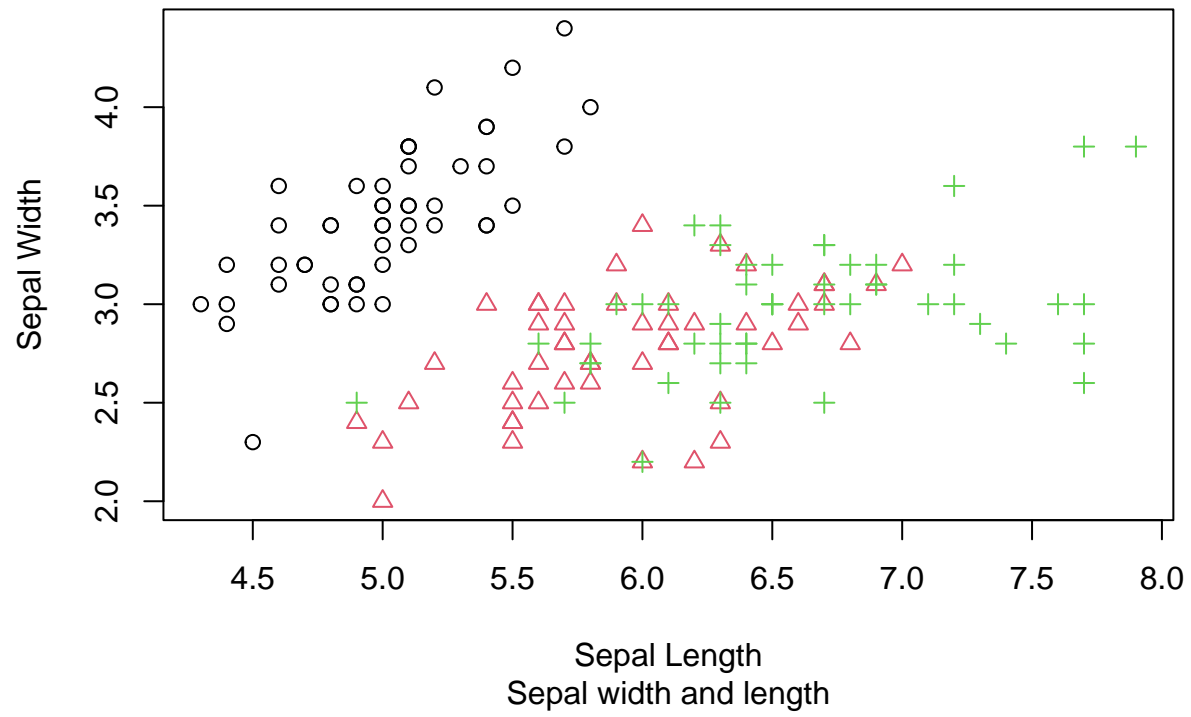
```
##      Sepal.Length Sepal.Width Petal.Length Petal.Width   Species
## 145          6.7         3.3         5.7         2.5 virginica
## 146          6.7         3.0         5.2         2.3 virginica
## 147          6.3         2.5         5.0         1.9 virginica
## 148          6.5         3.0         5.2         2.0 virginica
## 149          6.2         3.4         5.4         2.3 virginica
## 150          5.9         3.0         5.1         1.8 virginica
```

```
data(iris)
```

```
iris$Species <- as.factor(iris$Species)
```

```
plot(iris$Sepal.Length, iris$Sepal.Width,
     pch = as.integer(iris$Species),
     col = iris$Species,
     main = "Iris Dataset",
     sub = "Sepal width and length",
     xlab = "Sepal Length",
     ylab = "Sepal Width"
)
```

Iris Dataset



#The scatterplot shows similarities between the sepal width and length ranging from 5.5 to 7.0